EXHIBIT B

Claim Amendment: Pending Claims After Entry of Instant Amendment

21. (Thrice amended) A method for identifying the presence of cancerous cells in a human sample wherein said method comprises:

(a) determining the quantity of hTERT mRNA comprising β-region coding sequence in said sample and in a control sample of non cancerous cells by:

(1) contacting RNA from said sample and said control sample with a pair of primers, wherein said pair of primers consists of a first primer which hybridizes within exon 8 of the hTERT gene and a second primer which hybridizes upstream of exon 7 or downstream of exon 8 of the hTERT gene;

(3) measuring the generation of amplification products;

(4) determining the quantity of hTERT mRNA comprising β-region coding sequence in said sample from the results obtained in step (3); and

(b) identifying the presence of cancerous cells in said sample if the quantity of hTERT mRNA comprising β-region coding sequence in said sample is greater than the quantity of hTERT mRNA comprising β-region coding sequence in said control sample.

28. The method of Claim 21, wherein said second primer hybridizes upstream of exon 7 of the hTERT gene.

29. The method of Claim 28, wherein said second primer hybridizes within exon 6 of the hTERT gene.

30. The method of Claim 21, wherein said second primer is SYC1118 (SEQ ID NO:5), SYC1076 (SEQ ID NO:2) or SYC1078 (SEQ ID NO:3).

32. The method of Claim 21, wherein said first primer is SYC1097 (SEQ ID NO:4).

33. The method of Claim 21, wherein the second primer hybridizes within exon 9.

35. The method of Claim 21, wherein the amplification reaction is a polymerase chain reaction.

36. The method of Claim 21, wherein step (3) is carried out using a probe that is complementary or substantially complementary to said amplification products.

37. The method of Claim 36, wherein said probe is selected from the group consisting of CS12 (SEQ ID NO:6), CS1 (SEQ ID NO:7) and CS3 (SEQ ID NO:8).

46. The method of Claim 21, wherein step (2) additionally comprises amplifying the nucleic acid sequence in the presence of a probe which hybridizes to the nucleic acid sequence.

47. The method of Claim 46, wherein the probe is labeled.

50. (New) A method for identifying the presence of cancerous cells in a human sample wherein said method comprises:

(a) determining the quantity of hTERT mRNA comprising β-region coding sequence in said sample and in a control sample of non cancerous cells by:

(1) amplifying the β-region of the hTERT gene and said control sample;

(2) measuring the generation of amplification products;

(3) determining the quantity of hTERT mRNA comprising β-region coding sequence in said sample from the results obtained in step (2); and

(b) identifying the presence of cancerous cells in said sample if the quantity of hTERT mRNA comprising β-region coding sequence in said sample is greater than the quantity of hTERT mRNA comprising β-region coding sequence in said control sample.

51. (New) The method of Claim 50, wherein the amplification is carried out with a pair of primers, said pair of primers consists of a first primer which hybridizes upstream of

exon 8 of the hTERT gene and a second primer which hybridizes downstream of exon 8 of the hTERT gene.

52. (New) The method of Claim 51, wherein said first primer hybridizes within exon 6 of the hTERT gene and said second primer hybridizes within exon 9 of the hTERT gene.

53. (New) The method of Claim 52, wherein said first primer is SYC1076 (SEQ ID NO:2) and said second primer is SYC1078 (SEQ ID NO:3).